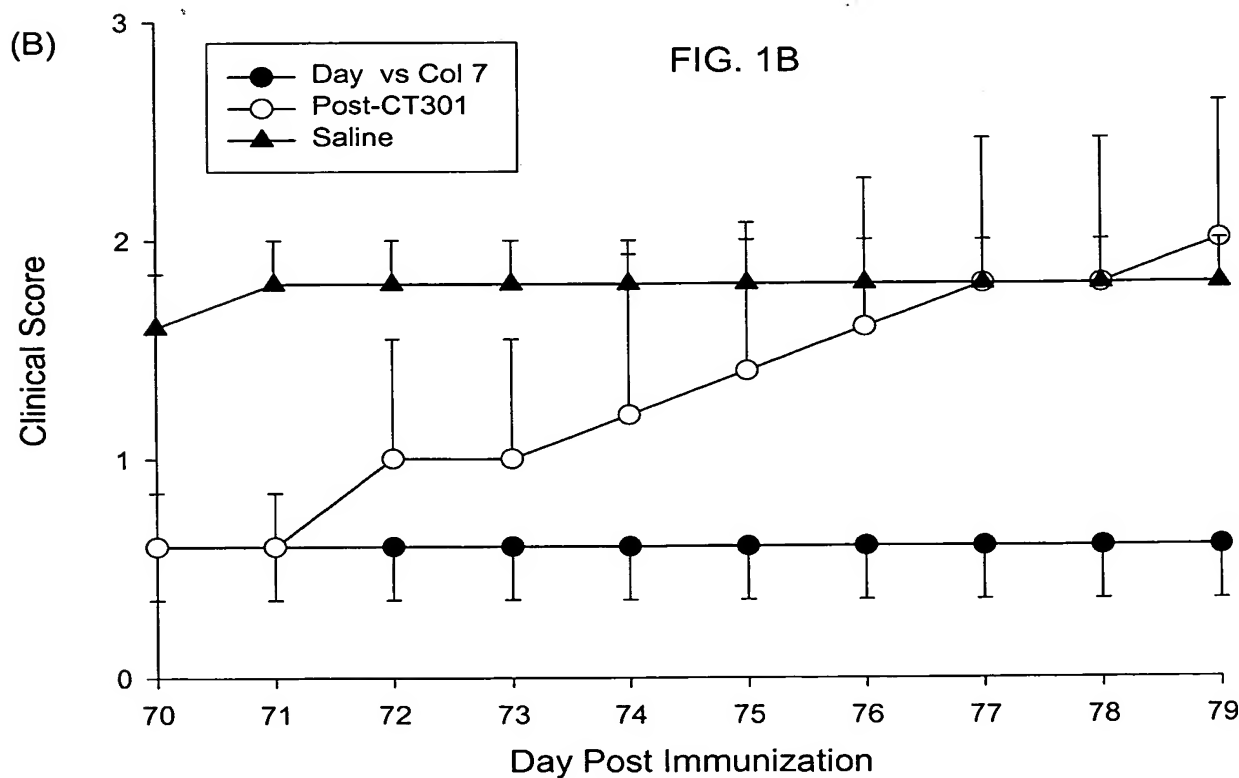
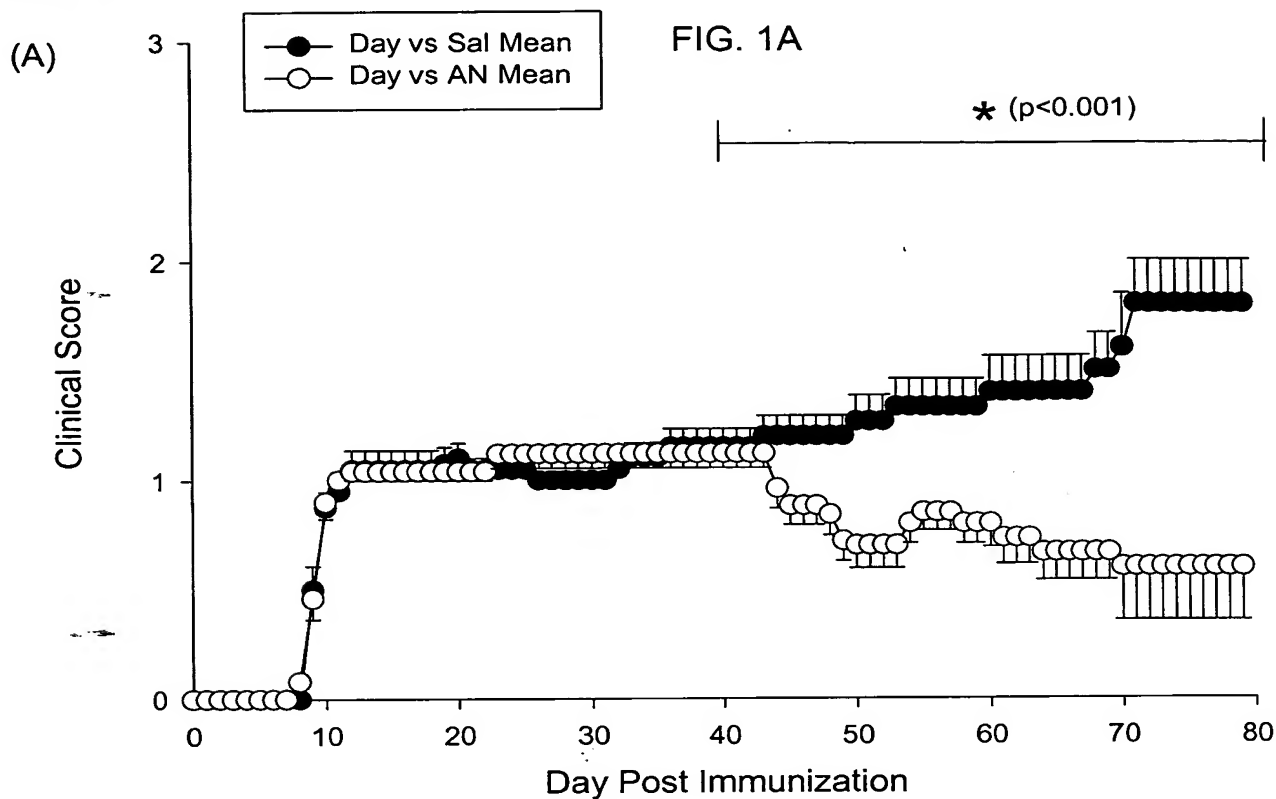




BEST AVAILABLE COPY



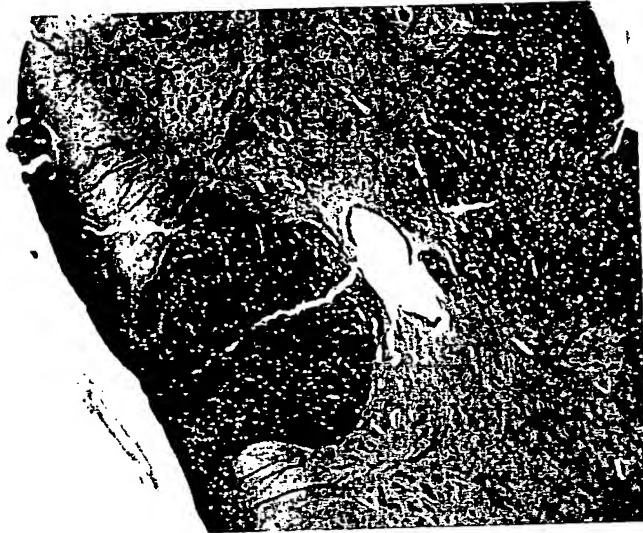


FIG. 2A

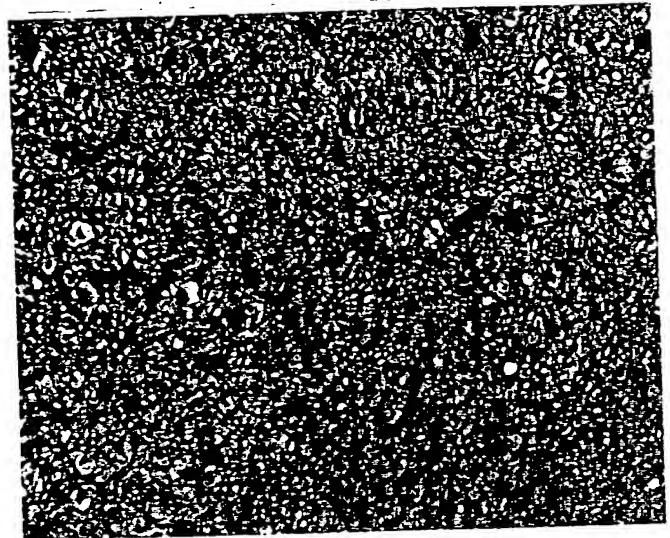


FIG. 2B



FIG. 2C

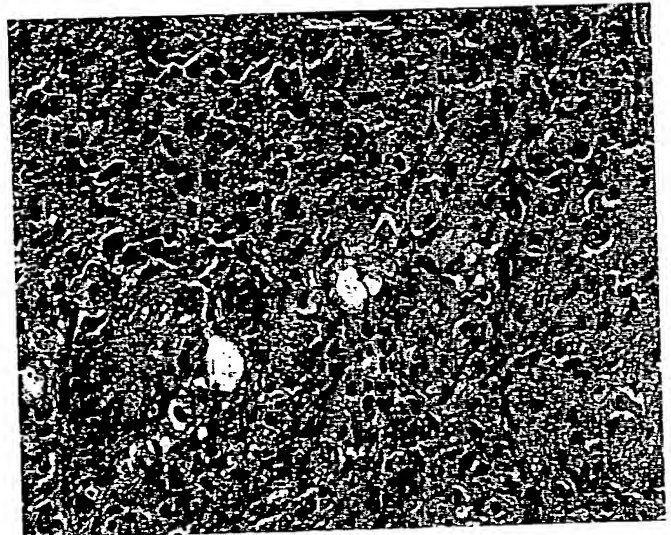


FIG. 2D



FIG. 2E

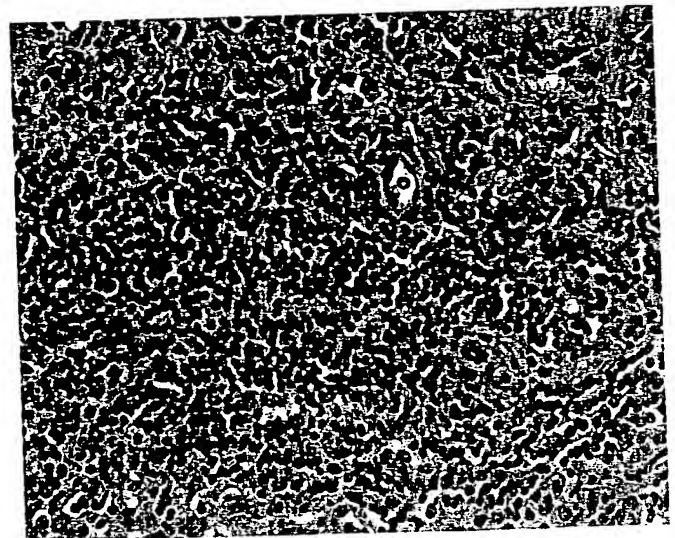


FIG. 2F

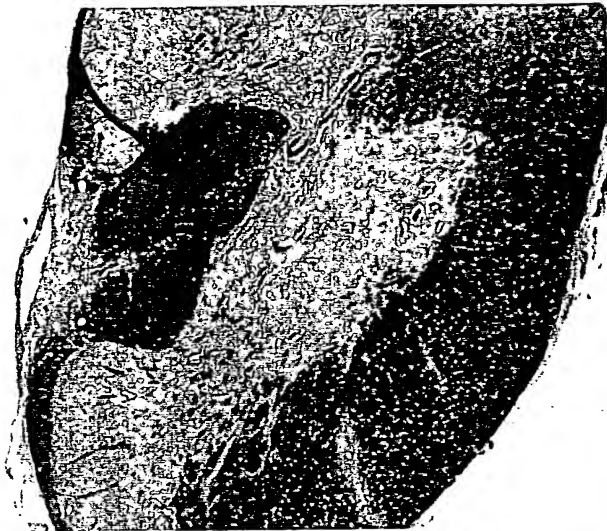


FIG. 2G

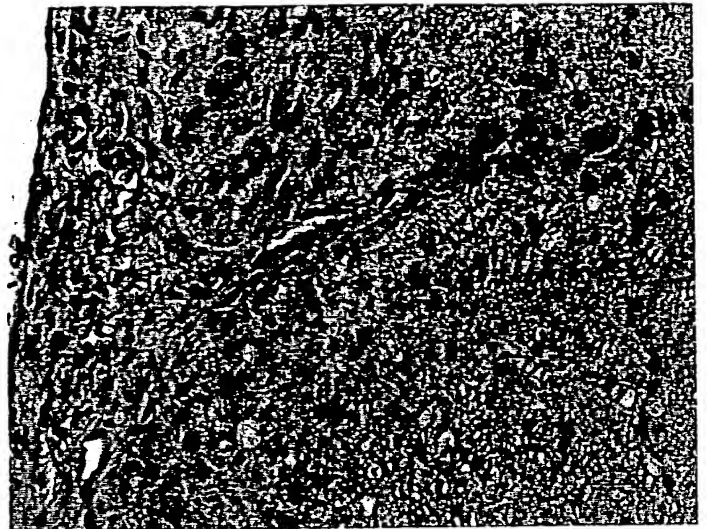


FIG. 2H

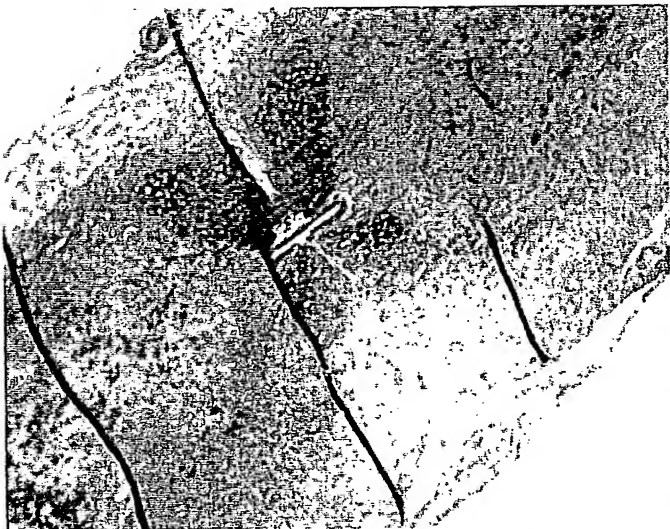


FIG. 2I

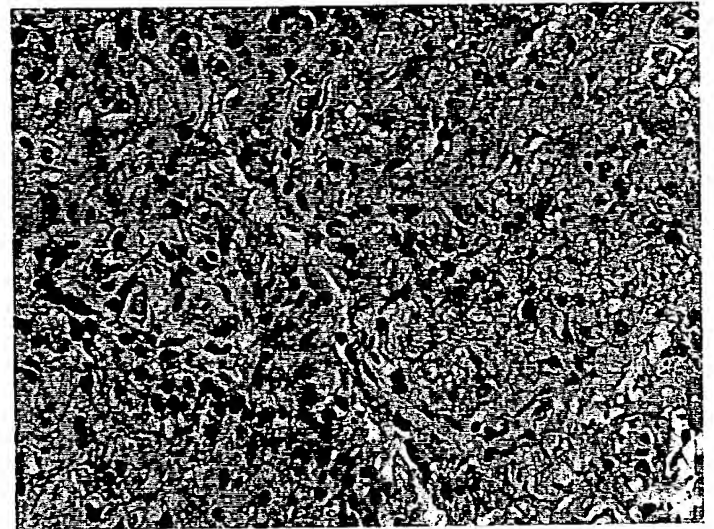


FIG. 2J



FIG. 2K

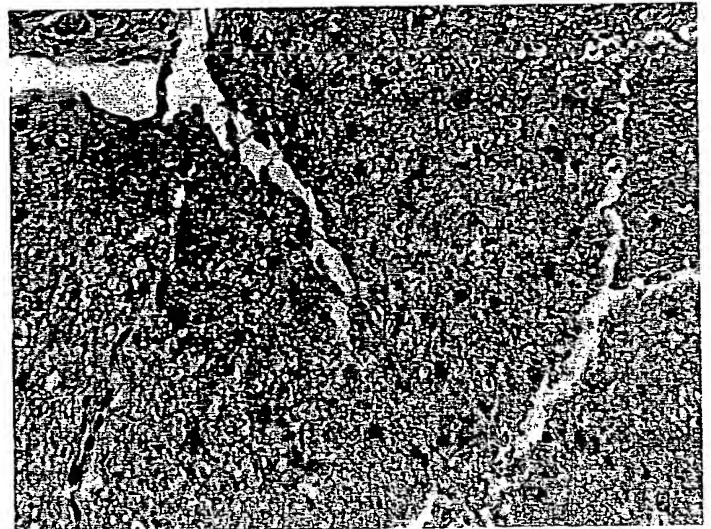
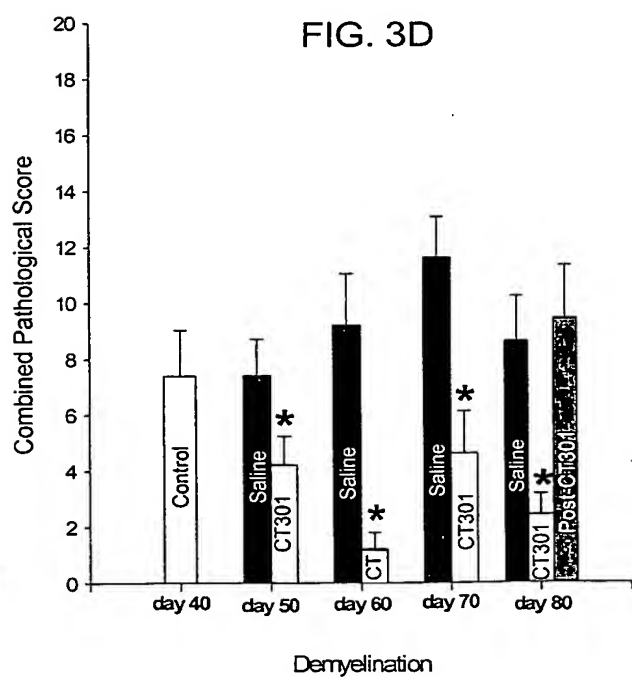
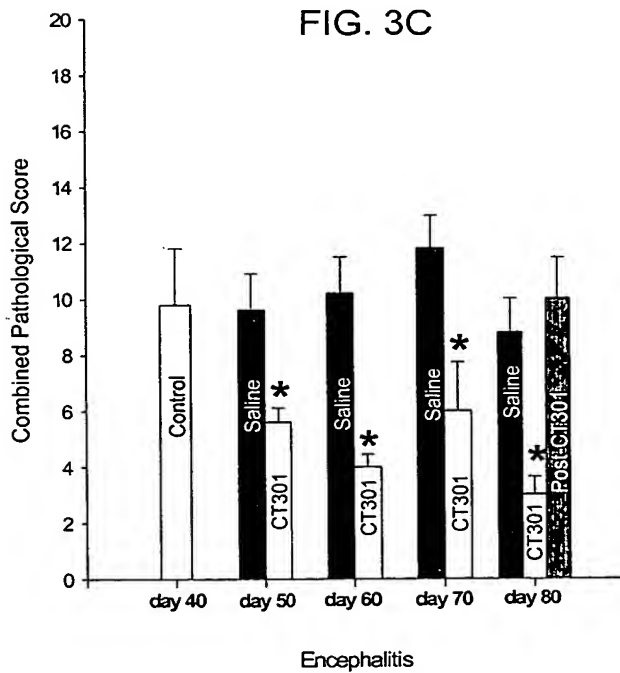
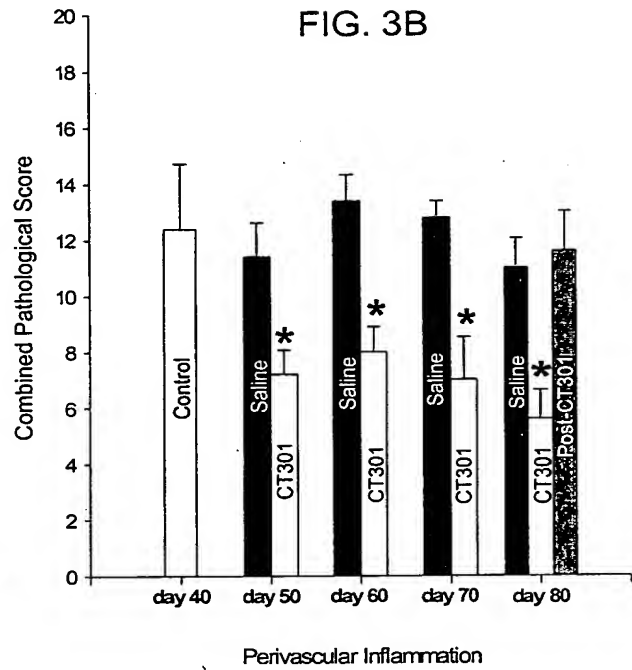
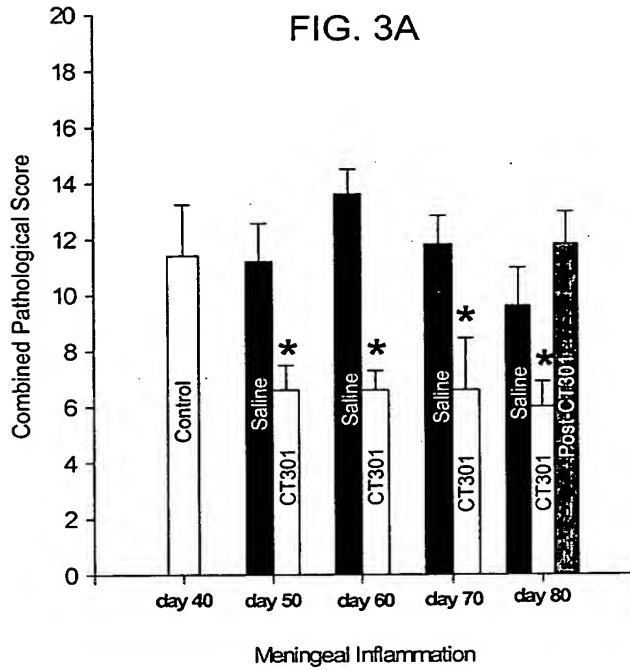


FIG. 2L



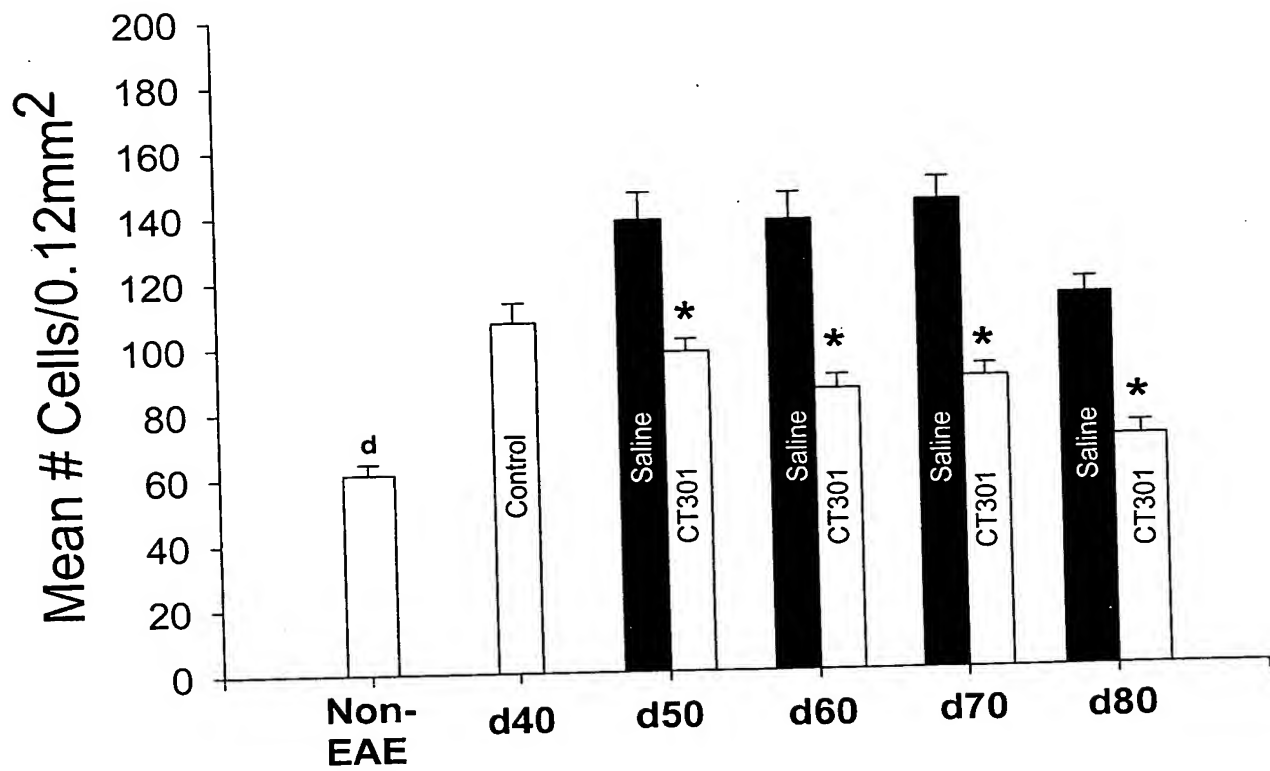
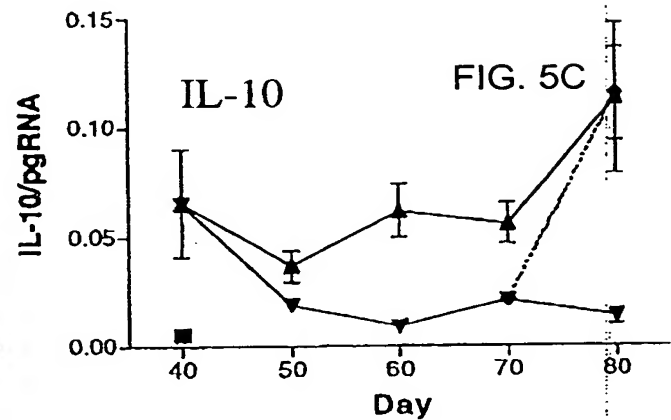
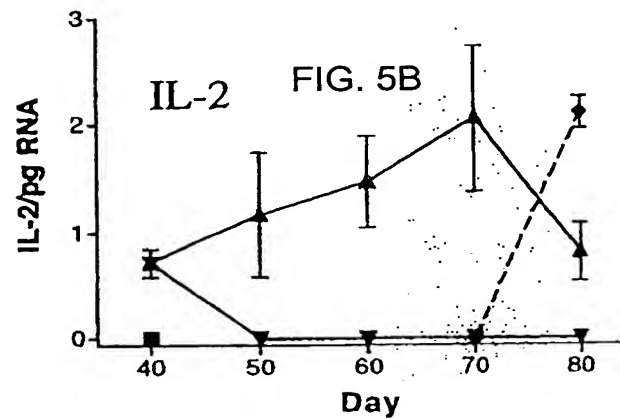
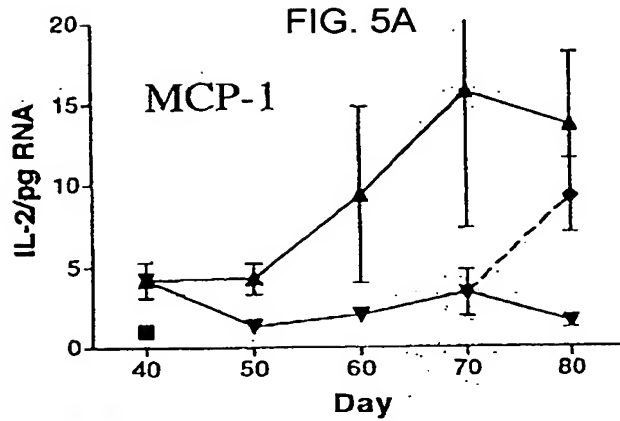
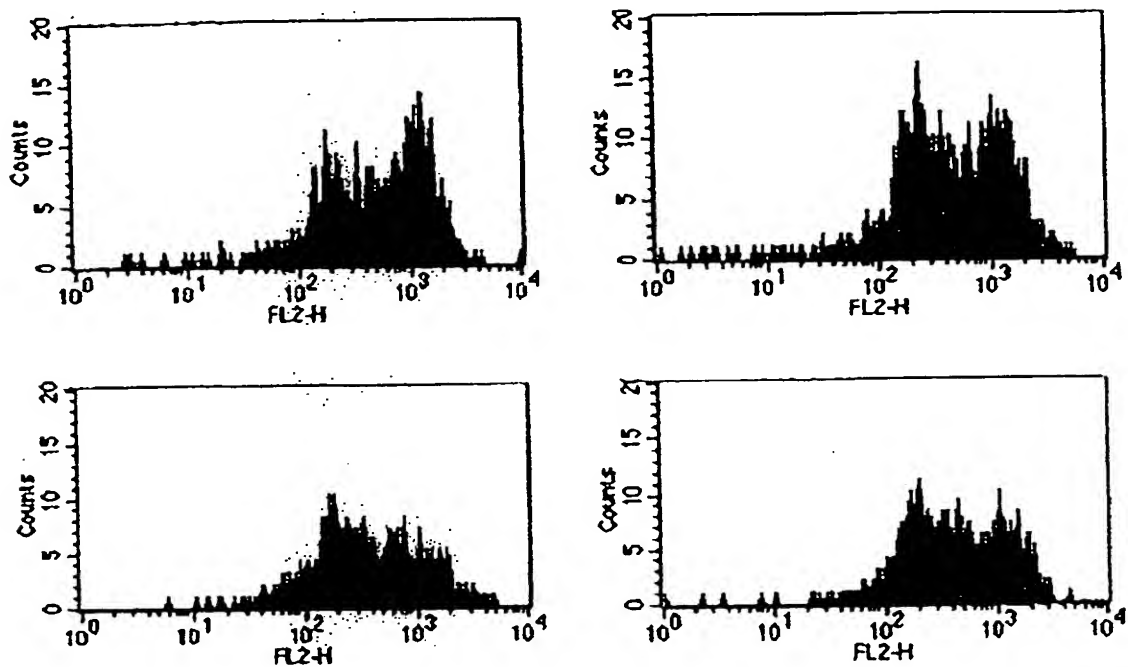


FIG. 4



CT301



Saline

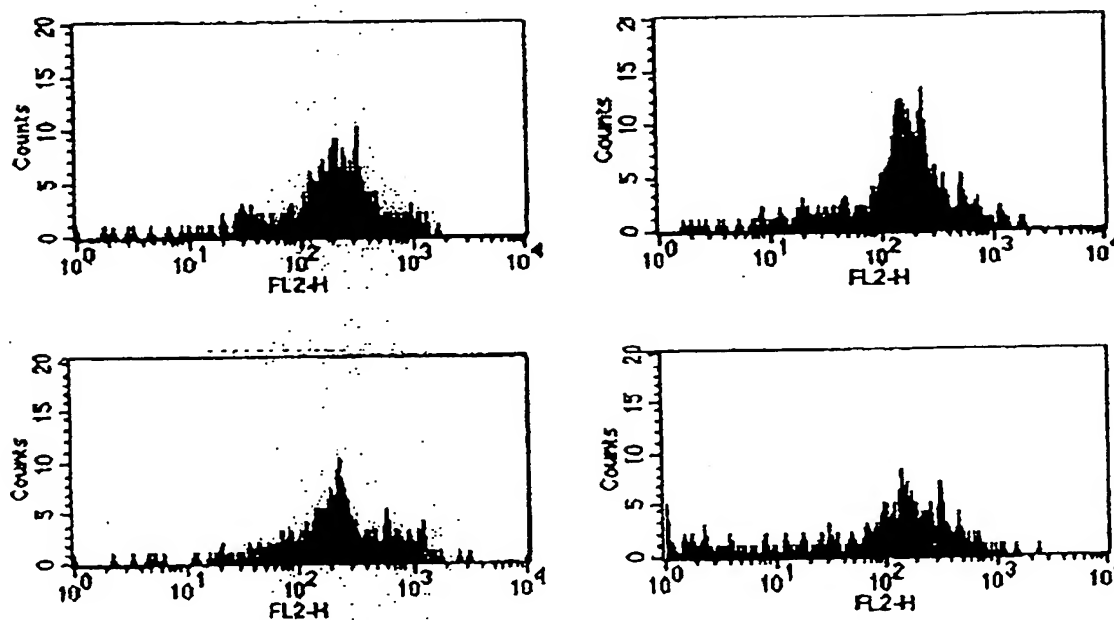


FIG. 6

Percentage $\alpha 4$ Integrin-High Blood Lymphocytes

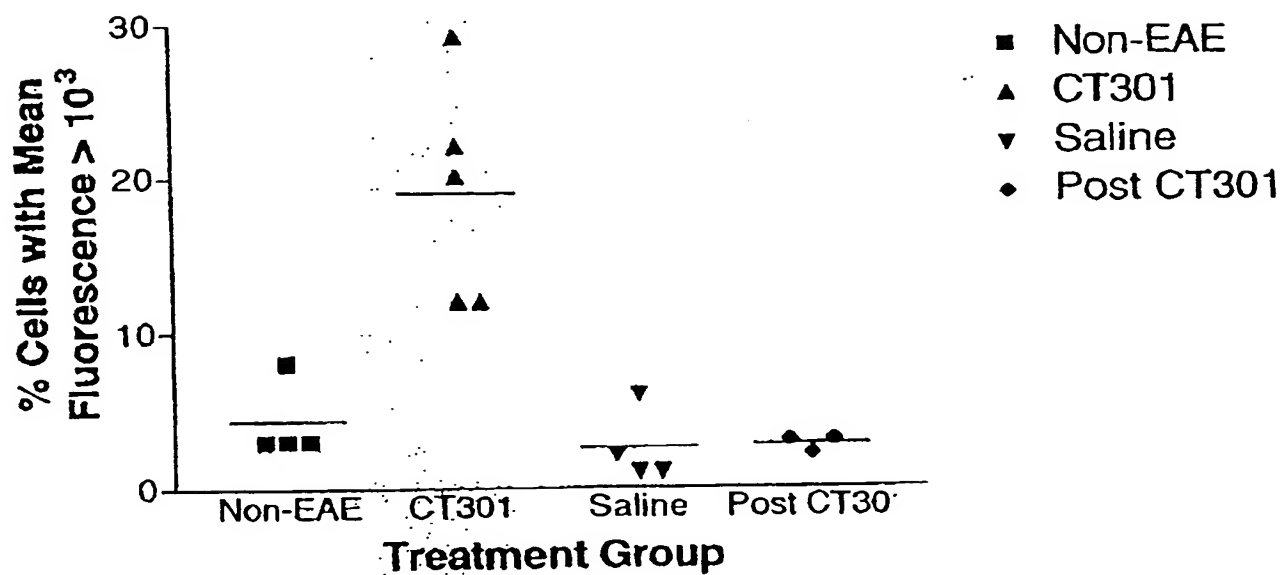


FIG. 7A

Expression of $\alpha 4$ Integrin on Blood Monocytes

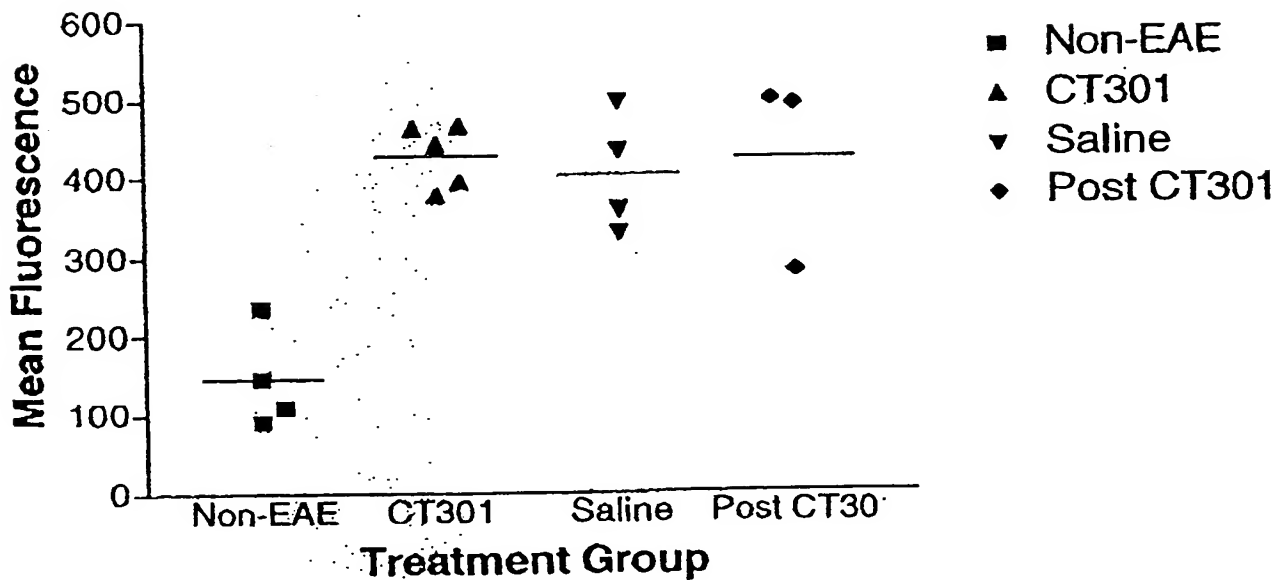


FIG. 7B

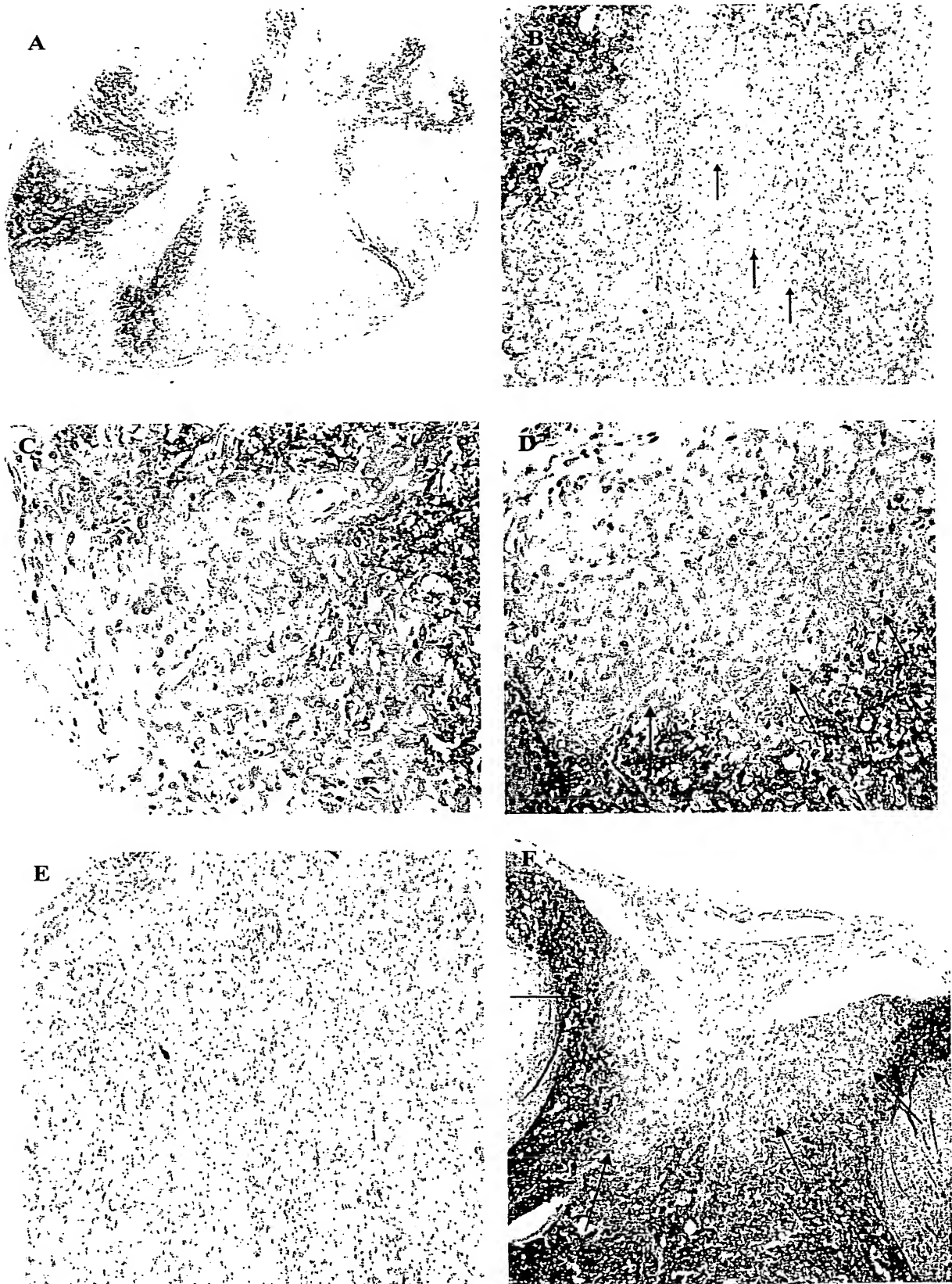


FIG. 8

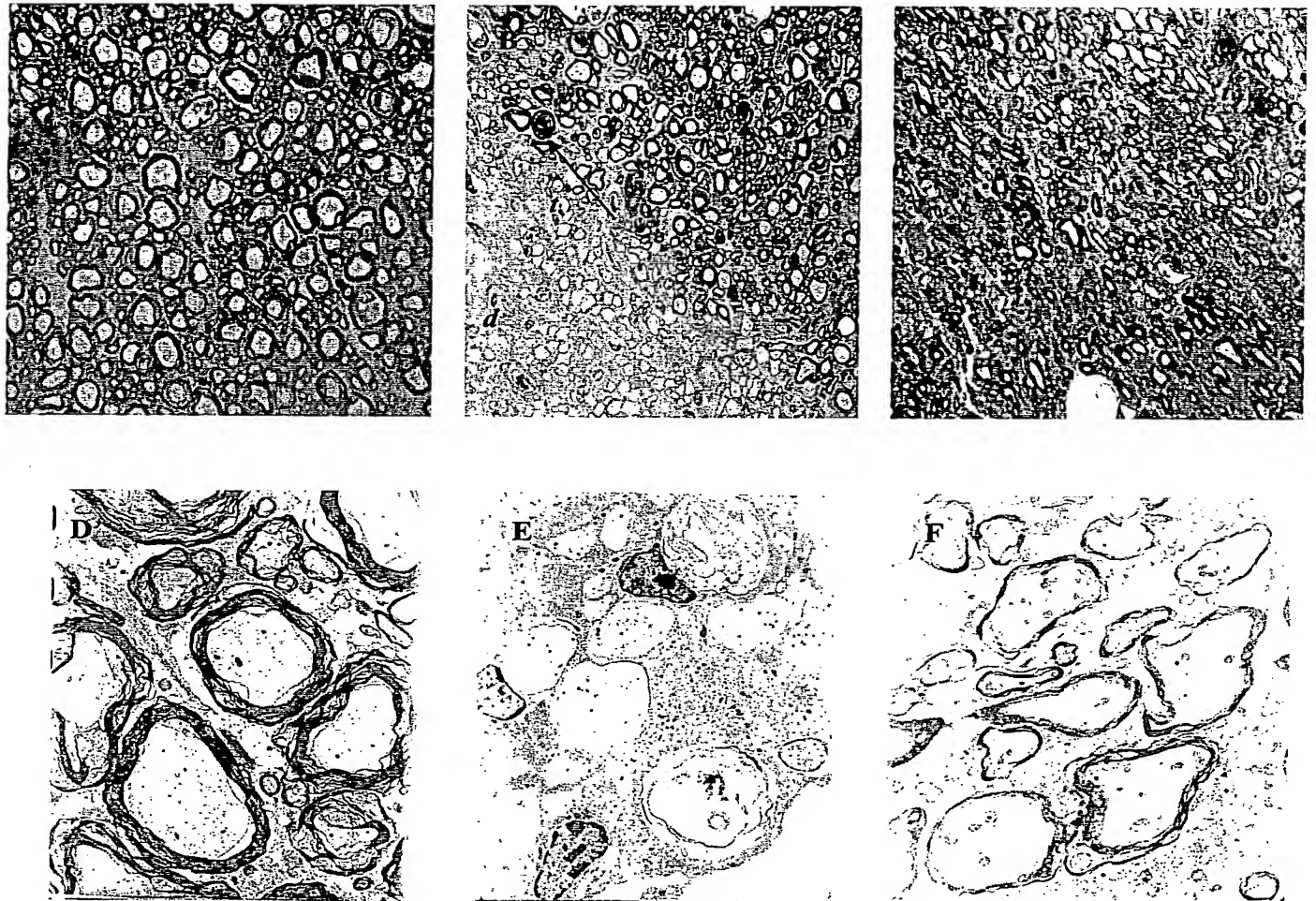


FIG. 9

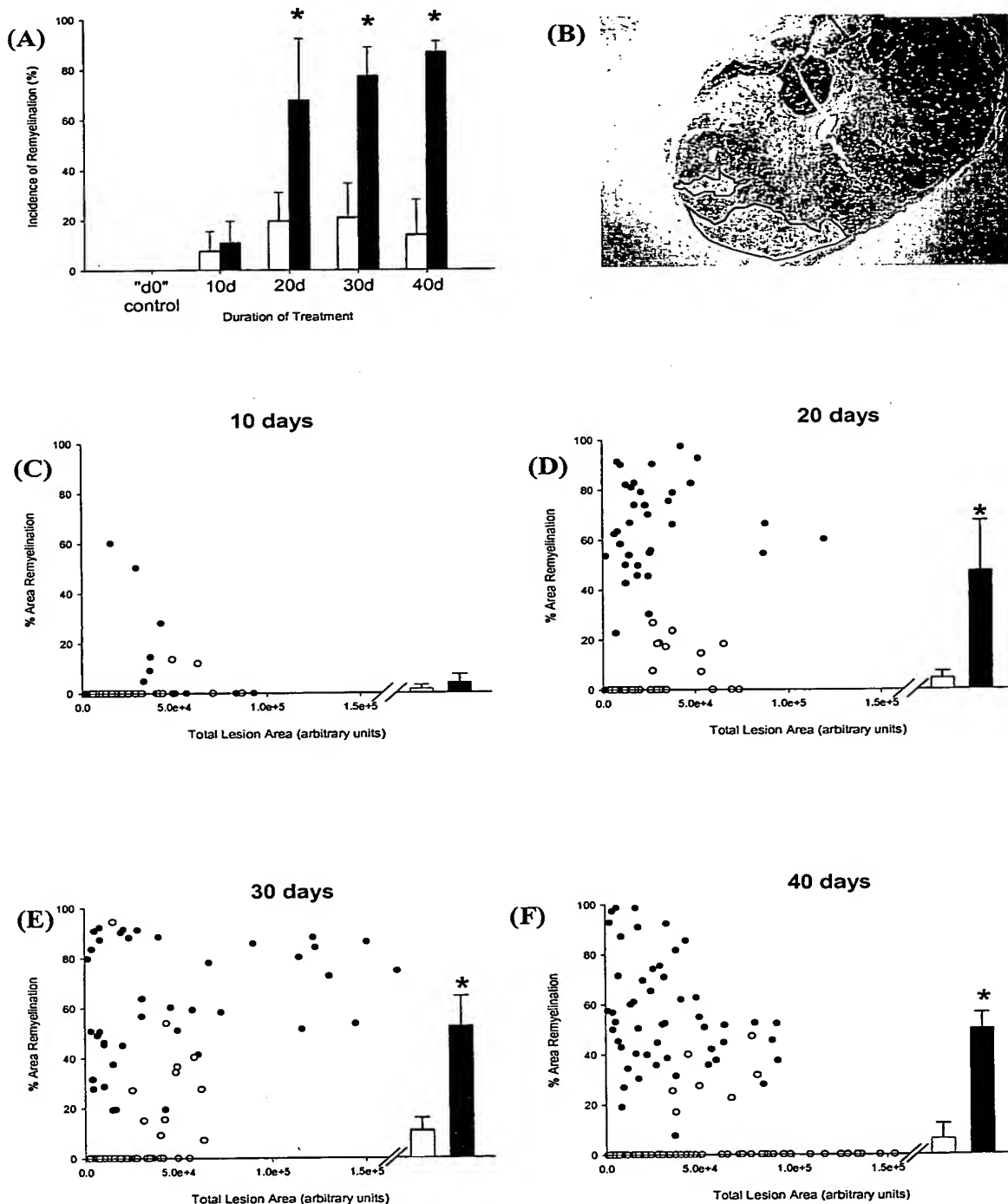


FIG. 10

1 atgagggccctgctcagatttttggattcttggtcaggagacgttgt

tactcccggggacgagtctaaaaacctaagaaccagtcctctgcaaca

49 agaaatgagaccgtctattcagttcctggggctcttggtgttctgggttcattg

tctttactctggcagataagtcaaggaccccgagaacaacaagaccgaagtacc

[M R P S I Q F L G L L L F W L H G
LEADER

103 tgctcagtggtgacatccagatgacacagtcctccatcctcactgtctgcatctct

acgagtcacactgtaggtctactgtgtcagaggtaggagtgacagacgtagaga

A Q C][D I Q M T Q S P S S L S A S L
FR1

157 gggaggcaagtaccatcacttgcaagacaagccaagacattaacaagtatat

ccctccgtttcagtggttagtgaacgttctgttcgggttctgtaattgttcata

G G K V T I T C][K T S Q D I N K Y M
CDR1

211 ggcttggtaccaacacaagcctggaaaacgtcctagggtgctcatacattacac

ccgaaccatggttggttcggaccttttgaggatccgacgagtatgtaattgtg

A][W Y Q H K P G K R P R L L I H][Y T
FR2

265 atctgcattacagccaggcatcccatcaagggttcagtggaagtgggtctgggag

tagacgtaattgtcgggtccgtagggtagttccaagtcaccttcacccagacctc

S A L Q P][G I P S R F S G S G S G R
CDR2

FIG. 11 A

319 agattattccttcaacatcagcaacctggagcctgaagatattgcaacttatta

tctaataagggaagtgtgtagtcgttggacctcggacttctataacggttgaaataat

D Y S F N I S N L E P E D I A T Y Y
FR3

373 ttgtctacagtatgataatctgtggacggttcggtggaggcaccaagctggaaat

aacagatgtcatactattagacacctgcaagccacctccgtgggttcgaccttta

C][L Q Y D N L W T][F G G G T K L E I
CDR3 FR4

427 caaacgggctgatgctgcaccaactgtatccatcttcccaccatccacccggga

gtttgcccgactacgacgtggttgacataggtagaagggtggttaggtgggacct

K]

AGG-5'
tcc
481 ---
agg

FIG. 11B

```
atgaaatgcagctgggtcatgtttcttctgatggcagtggttacaggg
1 -----
tactttacgtcgacccagttacaagaaggactaccgtcaccaatgtccc

      [M K C S W V M F F L M A V V T G
      LEADER

49  gtcaattcagaggttcagctgcagcagctctggggcagagcttgtgaagccaggg
-----
    cagttaagtctccaagtcgacgtcgtcagaccccgctctcgaacacttcggtccc
    V N S][E V Q L Q Q S G A E L V K P G
                                FR1

103  gcctcagtcgaagttgtcctgcacagcttctggcttcaacattaaagacacctat
-----
    cggagtcagttcaacaggacgtgtcgaagaccgaagttgtaatttctgtggata
    A S V K L S C T A S G F N I K][D T Y
                                CDR1

157  atacactgtgtgaagcagaggcctgaacagggcctggagtggttggaaggatt
-----
    tatgtgacacacttcgtctccggacttgtcccgacctcacctaaccttcctaa
    I H][C V K Q R P E Q G L E W I G][R I
                                FR2

211  gatcctgcgaatggttataactaaatatgacccgaagttccagggcaaggccact
-----
    ctaggacgcttaccaatatgatttatactgggcttcaagggtcccgttccggtga
    D P A N G Y T K Y D P K F Q G][K A T
                                CDR2

265  ataacagctgacacatcctccaacacagcctacctgcagctcagcagcctgaca
-----
    tattgtcgactgtgtaggaggttgtgtcggtatggacgtcgagtcgtcggactgt
    I T A D T S S N T A Y L Q L S S L T
                                FR3
```

FIG. 12A

319 tctgaggacactgccgtctatctctgtgctagagagggatattatggtaactac

agactcctgtgacggcagataaagacacgatctctccctataataaccattgatg

S E D T A V Y F C A R][E G Y Y G N Y
CDR3

373 ggggtctatgctatggactactggggtcaaggaacctcagtcaccgtctcctca

ccccagatacgataacctgatgaccccgagttccttgaggtcagtggcagaggagt

G V Y A M D Y][W G Q C T S V T V S S]

427 gccaaaacgacacccccatctgtctatccactggcccgggatcc

cggttttgctgtgggggtagacagataggtgaccgggcctagg

S S]

FIG. 12B

	FR1										CDR1										FR2										CDR2									
	1					2					3					4					5																			
	12345678901234567890123	45678901234	567890123456789	0123456																																				

21.6	DIQMTQSPSSLSASLGGKVTITC	KTSQDINKYMA	WYQHKPGKRPRLLIH	YTSALQP																																				
REI	DIQMTQSPSSLSASVGDRTITC	QASQDIKYLN	WYQQTGKAPKLLIY	EASNLQA																																				
La	DIQMTQSPSSLSASVGDRTITC	KTSQDINKYMA	WYQQTGKAPRLLIH	YTSALQP																																				
Lb	-----R-----																																							

	FR3										CDR3										FR4									
	6					7					8					9					10									
	78901234567890123456789012345678	901234567	8901234567																											

21.6	GIPSRFSGSGSGRDYSFNISNLEPEDIATYYC	LQYDNL-WT	FGGGTKLEIK																											
REI	GVPSRFSGSGSGTDYTFTISLQPEDIAATYYC	QQYQSLPYT	FGQGTLQIT																											
La	GIPSRFSGSGSGRDYTFTISLQPEDIAATYYC	LQYDNL-WT	FGQGTKVEIK																											
Lb	-I-----R-----VE-K																													

FIG. 13

	FR1										CDR1										FR2										CDR2									
	1					2					3					4					5					6														
	123456789012345678901234567890	12345	67890123456789	012A3456789012345																																				
	*****										*** *										*****																			
21.6	EVQLQQSGAELVKPGASVKLSCTASGFNIK	DTYIH	CVKQRPEQGLEWIG	RIDPANGYTKYDPKFQG																																				
2*CL	QVQLVQSGAEVKKPGASVKVSCKASGYTFT	SYAMH	WVRQAPGQRLEWMG	WINAGNGNTKYSQKFQG																																				
Ha	QVQLVQSGAEVKKPGASVKVSCKASGFNIK	DTYIH	WVRQAPGQRLEWMB	RIDPANGYTKYDPKFQG																																				
Hb	-----FNIK										-----G-----																													
Hc	-----FNIK										-----																													

	FR3										CDR3										FR4									
	7					8					9					10					11									
	67890123456789012ABC345678901234	567890ABCDEF12	34567890123																											
	*										*																			
21.6	KATITADTSSNTAYLQLSSLTSED	TAVYFCAR	EGYYGNYGVYAMDY	WGQGTSVTVSS																										
2*CL	RVTITRDTSASTAYMELSSLRSED	TAVYYCAR	GGYYGSGS----	NY WGQGTILVTVSS																										
Ha	RVTITADTSASTAYMELSSLRSED	TAVYYCAR	EGYYGNYGVYAMDY	WGQGTILVTVSS																										
Hb	-----A-----										-----																			
Hc	-----A-----										-----F-----																			

FIG. 14

HindIII KOZAK SEQUENCE

```
1  aagccttgccgccaccargagaccgtctattcagttcctggggctcttgttgttc
-----
   ttcgaacggcggtggtactctggcagataaagtcaaggaccccgagaacaacaag
               (M R P S I Q F L G L L L F
                               LEADER

55  tggcttcatggtgctcagtgtgacatccagatgacacagtcctccatcctcactg
-----
   accgaagtaccacgagtcacactgtaggtctactgtgtcagaggtaggagtgac
W L H G A Q C)(D I Q M T Q S P S S L
                               FR1

109 tctgcatctGTAggaGATAGagtcaccatcacttgcaagacaagccaagacatt
-----
   agacgtagaCATcctCTATCTcagtggtagtgaacgttctgttcggttctgtaa
S A S V G D R V T I T C)(K T S Q D I
                               CDR1

163 aacaagtatatggccttggtagctacaaCAGACacctggaaaaGCTcctagggtgctc
-----
   ttgttcatataccgaaccatgggttGTCTGTggaccttttCGAggatccgacgag
N K Y M A)(W Y Q Q T P G K A P R L L
                               FR2

217 atacattacacatctgcattacagccaggcatcccatcaagggttcagtgggaagt
-----
   tatgtaatgtgtagacgtaatgtcgggtccgtagggtagttccaagtcaccttca
I H)(Y T S A L Q P)(G I P S R F S G S
                               CDR2

271 gggctctgggagagattatACTttcACCAcagcAGCctgCAGcctgaagatatt
-----
   ccagaccctctctaataTGAaagTGGtagtcgTCGgacGTCggacttctataa
G S F R D Y T F T I S S L Q P E D I
                               FR3
```

FIG. 15A

325 gcaacttattattgtctacagtatgataatctgtggacgttcggtCAAggcacc

cgttgaataataacagatgtcatactattagacacctgcaagccaGTTccgtgg
A T Y Y C)[L Q Y D N L W T][F G Q G T
CDR3 FR4

SPLICE DONOR SITE BamHI
aagGTGgaaatcaaacgtgagrggatcc
379 -----
ttcCACcttttagtttgcaactcacctagg
K V E I K]

FIG. 15B

HindIII KOZAK SEQUENCE
AAGCTTGCCGCCACCATGGACTGGACCTGGCGCGTGTGTTTGCCTGCTCGCCGTG
1 -----
TTCGAACGGCGGTGGTACCTGACCTGGACCGCGCACAAAACGGACGAGCGGCAC
[M D W T W R V F C L L A V
LEADER
GCTCCTGGGGCCACAGCCAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAG
55 -----
CGAGGACCCCGGGTGTCTGGTCCACGTTGATCACGTCAGGCCGCGGCTTCACTTC
A P G A H S] [Q V Q L V Q S G A E V K
AAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAGCTAGCGGTTtcaacattaaa
109 -----
TTTGGGCCACGAAGGCACTTTTCAGTCGACATTTTCGATCGCCAAagttgtaattt
K P G A S V K V S C K A S G F N I K] [
FR1
gacacctatatacacTGGGTTAGACAGGCCCCCTGGCCAAaGGCTgGAGTGGATg
163 -----
ctgtggatatatgtgACCCAATCTGTCCGGgGaCCGGTTtCCGAcCTCACCTAc
D T Y I H] [W V R Q A P G Q R L E W M
CDR1 FR2

FIG. 16A

217 G Gaaggattgatcctgcgaatggttataactaaatatgacccgaagttccagggc

C Cttcctaactaggacgcttaccaatatgatttatactgggcttcaagggtcccg
G)[R I D P A N G Y T K Y D P K F Q G)]
CDR2

271 cgggtcACCCatcACCgcaGACACCTCTgccagcACCGCCTACATGGAAGTGTCC

gcccagTGGtagTGGcgtCTGTGGAGAcgggtcgTGGCGGATGTACCTTGACAGG
R V T I T A D T S A S T A Y M E L S
FR3

325 AGCCTGCGCTCCGAGGACACTGCAGTCTACTACTGCGCCagagaggggatattat

TCGGACGCGAGGCTCCTGTGACGTCAGATGATGACGCGGtctctccctataata
S L R S E D T A V Y Y C A R)](E G Y Y
ggtaactacggggtctatgctatgGACTActGGGGtCAaGGaACCCTTGTCCACC
379 -----
ccattgatgccccagatacagatacCTGATgACCCCaGTtCctTGGGAACAGTGG
G N Y G V Y A M D Y)](W G Q G T L V T
CDR3 FR4

433 SPLICE DONOR SITE BamHI
GTctcctCAGGTGAGTGGATCC

CAGaggAGTCCACTCACCTAGG
V S S]

FIG. 16B

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys - C

FIG. 17A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ser Leu Val Xaa
Xaa Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
Tyr Asn Ser Leu Pro Glu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
Ile Lys - C

FIG. 17B

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

N - Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe
Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
Ala Arg Gly Tyr Tyr Tyr Tyr Asp Ser Xaa Val Gly Tyr Tyr Ala Met
Asp Tyr Trp Gly Gln Gly Thr Xaa Val Thr Val Ser Ser - C

FIG. 18A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
Gly Trp Ile Asn Pro Tyr Gly Asn Gly Asp Thr Asn Tyr Ala Gln Lys
Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
Cys Ala Arg Ala Pro Gly Tyr Gly Ser Gly Gly Gly Cys Tyr Arg Gly Asp
Tyr Xaa Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser - C

FIG. 18B

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☒ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.